



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 181503

TO: James Schultz
Location: rem/2D18/2C18
Art U.: 1035
Wednesday, March 15, 2006

Case Serial Number: 10/726422

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Sea

Examiner Schultz,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
REM-1A65
571-272-2527

schulwitz@uspto.gov

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181503
ME

STIC-Biotech/ChemLib

From: Schultz, James
Sent: Monday, March 06, 2006 5:25 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 10/726,422

Hello,

Could you please run a standard, length limited nucleotide sequence search against SEQ ID NO: 1 in the above entitled application, which returns hits between 10 and 40 nucleotides?

Thanks,
Doug Schultz

James Douglas Schultz, PhD
Primary Examiner
AU 1635 (Biotechnology)
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

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MAR - 7 2006
(SIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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SUMMARIES									
result No.	Score	Query Match	Length	DB ID	Description	Score	Match	Length	DB ID
1	24	5.8	24	6	AR028459 Sequence	5.8*	Score 24;	DB 6;	Length 24;
c	2	24	5.8	24	6 AR028460 Sequence	5.8*	Score 24;	DB 6;	Length 24;
c	3	24	5.8	24	6 AR052451 Sequence	5.8*	Score 24;	DB 6;	Length 24;
c	4	24	5.8	24	6 AR052452 Sequence	5.8*	Score 24;	DB 6;	Length 24;
c	5	24	5.8	24	6 I63533 Sequence 8	5.8*	Score 24;	DB 6;	Length 24;
c	6	24	5.8	24	6 I63534 Sequence 9	5.8*	Score 24;	DB 6;	Length 24;
c	7	24	5.8	24	6 I89355 Sequence 8	5.8*	Score 24;	DB 6;	Length 24;
c	8	24	5.8	24	6 I89356 Sequence 9	5.8*	Score 24;	DB 6;	Length 24;
c	9	24	5.8	24	6 AR370452 Sequence	5.8*	Score 24;	DB 6;	Length 24;
c	10	24	5.8	24	6 AR370453 Sequence	5.8*	Score 24;	DB 6;	Length 24;
c	11	24	5.8	24	6 AX645186 Sequence	5.8*	Score 24;	DB 6;	Length 24;
c	12	24	5.8	24	6 AX645187 Sequence	5.8*	Score 24;	DB 6;	Length 24;
c	13	20.4	5.0	36	6 I69104 Sequence 37	5.0*	Score 24;	DB 6;	Length 24;
c	14	20.4	5.0	36	6 AR253702 Sequence	5.0*	Score 24;	DB 6;	Length 24;
c	15	20.4	5.0	36	6 AX696757 Sequence	5.0*	Score 24;	DB 6;	Length 24;
c	16	20.2	4.9	25	6 AX556577 Sequence	4.9*	Score 24;	DB 6;	Length 24;
c	17	19.6	4.8	40	6 AX352153 Sequence	4.8*	Score 24;	DB 6;	Length 24;
c	18	19.2	4.7	33	6 AR099439 Sequence	4.7*	Score 24;	DB 6;	Length 24;

TITLE Patent: US 588881-A 4 12-JAN-1999; FEATURES source	Method for prognosis of prostate cancer									
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Qy	356	ACCCTAGCTGAAGTTCAGCAATT	379							
Db	24	ACCCTAGCTGAAGTTCAGCAATT	1							
RESULT 3										
AR052451	AR052451	Sequence 8 from patent US 5831033.	24 bp	DNA	linear	PAT 29-SEP-1999	ORIGIN			
DEFINITION							Query Match	5.8%;	Score 24;	DB 6;
ACCESSION	AR052451						Best Local Similarity	100.0%;	Pred. No. 4.6e+05;	Length 24;
VERSION	AR052451.1	GI:5975815					Matches	24;	Conservative	0;
KEYWORDS	.						Mismatches	0;	Indels	0;
SOURCE	Unknown.								Gaps	0;
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 24)									
AUTHORS	Zetter,B.R. and Bao,L.									
TITLE	Human thymosin .beta.15 gene, protein and uses thereof									
JOURNAL	Patent: US 5831033-A 8 03-NOV-1998;									
FEATURES	Location/Qualifiers									
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Best Local Similarity	100.0%;	Pred. No. 4.6e+05;								
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Qy	1	TATCAGCTAGTGGCTGACCCGG	24				Query Match	5.8%;	Score 24;	DB 6;
Db	1	TATCAGCTAGTGGCTGACCCGG	24				Best Local Similarity	100.0%;	Pred. No. 4.6e+05;	Length 24;
RESULT 6							Matches	24;	Conservative	0;
AR05334/c	AR05334/c	Sequence 9 from patent US 5663071.	24 bp	DNA	linear	PAT 07-OCT-1997	ORIGIN			
DEFINITION							Query Match	5.8%;	Score 24;	DB 6;
ACCESSION	AR05334						Best Local Similarity	100.0%;	Pred. No. 4.6e+05;	Length 24;
VERSION	AR05334.1	GI:2481107					Matches	24;	Conservative	0;
KEYWORDS	.						Mismatches	0;	Indels	0;
SOURCE	Unknown.								Gaps	0;
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 24)									
AUTHORS	Zetter,B.R. and Bao,L.									
TITLE	Human thymosin .beta.15 gene, protein and uses thereof									
JOURNAL	Patent: US 5663071-A 9 02-SEP-1997;									
FEATURES	Location/Qualifiers									
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Best Local Similarity	100.0%;	Pred. No. 4.6e+05;								
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Qy	356	ACCTGACTGAAAGTCAGCAATT	379				Query Match	5.8%;	Score 24;	DB 6;
Db	24	ACCTGACTGAAAGTCAGCAATT	1				Best Local Similarity	100.0%;	Pred. No. 4.6e+05;	Length 24;
RESULT 7							Matches	24;	Conservative	0;
AR05355	AR05355	Sequence 8 from patent US 5722133.	24 bp	DNA	linear	PAT 10-AUG-1998	ORIGIN			
DEFINITION							Query Match	5.8%;	Score 24;	DB 6;
ACCESSION	AR05355						Best Local Similarity	100.0%;	Pred. No. 4.6e+05;	Length 24;
VERSION	AR05355.1	GI:3409295					Matches	24;	Conservative	0;
KEYWORDS	.						Mismatches	0;	Indels	0;
SOURCE	Unknown.								Gaps	0;
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 24)									
AUTHORS	Zetter,B.R. and Bao,L.									
TITLE	Human thymosin .beta.15									
JOURNAL	Patent: US 5831033-A 9 03-NOV-1998;									
FEATURES	Location/Qualifiers									
source	1. .24									
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Db	24	ACCCTAGCTGAAGTTCAGCAATT	1				Best Local Similarity	100.0%;	Pred. No. 4.6e+05;	Length 24;

JOURNAL	Patent: US 5721337-A 8 24-FEB-1998; Location/Qualifiers 1. .24 /organism="unassigned" DNA"	Db	1 TATCAGCTAGTGGCTGCCACCGCG 24
ORIGIN			
FEATURES		RESULT 10 AR370453/C LOCUS Sequence 9 from Patent US 6300479. DEFINITION AR370453 VERSION AR370453.1 GI:34607138 KEYWORDS Unknown. ORGANISM Unknown. SOURCE Unknown.	linear PAT 12-SEP-2003
source		REFERENCE 1 (bases 1 to 24) AUTHORS Zetter, B.R. and Bao, L. TITLE Human thymosin .beta.15 JOURNAL Patent: US 5721337-A 9 24-FEB-1998; FEATURES Location/Qualifiers source 1. .24 /organism="unassigned" DNA"	
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Qy	1 TATCAGCTAGTGGCTGCCACCGCG 24	Db	1 TATCAGCTAGTGGCTGCCACCGCG 24
Db	1 TATCAGCTAGTGGCTGCCACCGCG 24	Db	1 TATCAGCTAGTGGCTGCCACCGCG 24
RESULT 8			
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VERSION	189356	ORIGIN	
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SOURCE		REFERENCE 1 (bases 1 to 24) AUTHORS Zetter, B.R. and Bao, L. TITLE Human thymosin .beta.15 JOURNAL Patent: US 5721337-A 9 24-FEB-1998; FEATURES Location/Qualifiers source 1. .24 /organism="unassigned" DNA"	
ORGANISM	Unknown.	Db	1 TATCAGCTAGTGGCTGCCACCGCG 24
RESULT 8			
LOCUS	Sequence 9 from Patent US 5721337.	JOURNAL	Query Match 5.8%; Score 24; DB 6; Length 24; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DEFINITION		FEATURES	
ACCESSION	189356	source 1. .24 /organism="unassigned" DNA"	
VERSION	189356	ORIGIN	
KEYWORDS		Query Match 5.8%; Score 24; DB 6; Length 24; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
SOURCE		REFERENCE 1 (bases 1 to 24) AUTHORS Zetter, B.R. and Bao, L. TITLE Human thymosin .beta.15 JOURNAL Patent: US 5721337-A 9 24-FEB-1998; FEATURES Location/Qualifiers source 1. .24 /organism="unassigned" DNA"	
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VERSION	AX645186.1 GI:28611008	ORIGIN	
KEYWORDS		Query Match 5.8%; Score 24; DB 6; Length 24; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
SOURCE		REFERENCE 1 (bases 1 to 24) AUTHORS Zetter, B.R. and Bao, L. TITLE Thymosin B15 as a marker in diagnosis and prognosis of cancer JOURNAL Patent: EP 1270745-A 3 02-FEB-2003; FEATURES Location/Qualifiers source 1. .24 /db_xref="taxon:32644"	
ORGANISM	unclassified sequences.	Db	1 TATCAGCTAGTGGCTGCCACCGCG 24
RESULT 9			
LOCUS	Sequence 3 from Patent EP1270745.	JOURNAL	Query Match 5.8%; Score 24; DB 6; Length 24; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DEFINITION		FEATURES	
ACCESSION	AX645186	source 1. .24 /organism="unassigned" DNA"	
VERSION	AX645186.1 GI:28611008	ORIGIN	
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SOURCE		REFERENCE 1 (bases 1 to 24) AUTHORS Zetter, B.R. and Bao, L. TITLE Thymosin B15 as a marker in diagnosis and prognosis of cancer JOURNAL Patent: EP 1270745-A 3 02-FEB-2003; FEATURES Location/Qualifiers source 1. .24 /db_xref="taxon:32644"	
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LOCUS	Sequence 8 from Patent US 6300479.	JOURNAL	Query Match 5.8%; Score 24; DB 6; Length 24; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DEFINITION		FEATURES	
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VERSION	AR370452.1 GI:34607137	ORIGIN	
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SOURCE		REFERENCE 1 (bases 1 to 24) AUTHORS Zetter, B.R. and Bao, L. TITLE Antibodies specific for human thymosin .beta.15 protein and uses JOURNAL Patent: US 6300479-A 8 09-OCT-2001; FEATURES Location/Qualifiers source 1. .24 /organism="unassigned" DNA"	
ORGANISM	Unknown.	Db	1 TATCAGCTAGTGGCTGCCACCGCG 24
RESULT 12			
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DEFINITION		FEATURES	
ACCESSION	AX645187	source 1. .24 /organism="unassigned" DNA"	
VERSION	AX645187.1 GI:28611009	ORIGIN	
KEYWORDS		Query Match 5.8%; Score 24; DB 6; Length 24; Best Local Similarity 100.0%; Pred. No. 4.6e+05; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
SOURCE		REFERENCE 1 (bases 1 to 24) AUTHORS Zetter, B.R. and Bao, L. TITLE Antibodies specific for human thymosin .beta.15 protein and uses JOURNAL Patent: US 6300479-A 8 09-OCT-2001; FEATURES Location/Qualifiers source 1. .24 /organism="unassigned" DNA"	
ORGANISM	unclassified sequences.	Db	1 TATCAGCTAGTGGCTGCCACCGCG 24

ORGANISM	unidentified sequences.	FEATURES	Pharmacia Corporation; St. Louis, MO
REFERENCE	1	Source	1..36
AUTHORS	Zetter, B.R. and Bao, L.		/organism="unknown"
JOURNAL	Thymosin B15 as a marker in diagnosis and prognosis of cancer		/mol_type="unassigned DNA"
TITLE	Patent: EP 1270745-A 02-JAN-2003;		
FEATURES	CHILDREN'S MEDICAL CENTER CORPORATION (US)		
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Best Local Similarity	100.0%; Pred. No. 4.6e+05;	Best Local Similarity	80.0%; Pred. No. 3.1e+06;
Matches	24; Conservative 0; Mismatches 0;	Matches	24; Conservative 0; Mismatches 6;
Indels	0;	Indels	0;
Gaps	0;	Gaps	0;
RESULT 13		Query Match	5.0%; Score 20.4; DB 6; Length 36;
LOCUS	169104	Best Local Similarity	80.0%; Pred. No. 3.1e+06;
DEFINITION	Sequence 374 from patent US 5677149.	Matches	24; Conservative 0; Mismatches 6;
ACCESSION	169104	Indels	0;
VERSION	24	Gaps	0;
KEYWORDS		Query Match	5.0%; Score 20.4; DB 6; Length 36;
SOURCE	Unknown.	Best Local Similarity	80.0%; Pred. No. 3.1e+06;
ORGANISM	Unclassified.	Matches	24; Conservative 0; Mismatches 6;
REFERENCE	1 (bases 1 to 36)	Indels	0;
AUTHORS	Bauer, S., Chistopher, Abrams, M., Allen,., Bradford-Goldberg, S., Ruth, ., Caparon, M., Helena,., Easton, A., Michael,., Klein, B., Kure, ., McKearn, J., Patrick, ., Ollins, P., Paik, K., Polazzi, J., and Thomas, J. W., Warren, J., Warren.	Gaps	0;
TITLE	Interleukin-3 (IL-3) mutant polypeptides and their recombinant production	Query Match	5.0%; Score 20.4; DB 6; Length 36;
JOURNAL	Patent: US 5677149-A 374 14-OCT-1997;	Best Local Similarity	80.0%; Pred. No. 3.1e+06;
FEATURES	Location/Qualifiers	Matches	24; Conservative 0; Mismatches 6;
source	1..36	Indels	0;
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Query Match	5.0%; Score 20.4; DB 6; Length 36;	Matches	24; Conservative 0; Mismatches 6;
Best Local Similarity	80.0%; Pred. No. 3.1e+06;	Indels	0;
Matches	24; Conservative 0; Mismatches 6;	Gaps	0;
Indels	0;	Query Match	5.0%; Score 20.4; DB 6; Length 36;
Gaps	0;	Best Local Similarity	80.0%; Pred. No. 3.1e+06;
Db	31	Matches	24; Conservative 0; Mismatches 6;
		Indels	0;
		Gaps	0;
RESULT 14		Query Match	5.0%; Score 20.4; DB 6; Length 36;
LOCUS	AR253702	Best Local Similarity	80.0%; Pred. No. 3.1e+06;
DEFINITION	Sequence 374 from patent US 6479261.	Matches	24; Conservative 0; Mismatches 6;
ACCESSION	AR253702	Indels	0;
VERSION	AR253702.1	Gaps	0;
KEYWORDS	Unknown.	Query Match	5.0%; Score 20.4; DB 6; Length 36;
SOURCE	Unclassified.	Best Local Similarity	80.0%; Pred. No. 3.1e+06;
ORGANISM	Unknown.	Matches	24; Conservative 0; Mismatches 6;
REFERENCE	1 (bases 1 to 36)	Indels	0;
AUTHORS	Bauer, S.C., Abrams, M.A., Bradford-Goldberg, S.R., Caparon, M.H., Easton, A.M., Klein, B.K., McKearn, J.P., Ollins, P., Paik, K., Polazzi, J., and Thomas, J. W.	Gaps	0;
TITLE	Methods of using interleukin-3 (IL-3) mutant polypeptides for ex-vivo expansion of hematopoietic stem cells	Query Match	5.0%; Score 20.4; DB 6; Length 36;
JOURNAL	Patent: US 6479261-A 374 12-NOV-2002;	Best Local Similarity	80.0%; Pred. No. 3.1e+06;

Search completed: March 12, 2006, 06:43:56

Job time : 27.4 secs

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OM nucleic - nucleic search, using SW model

Run on: March 12, 2006, 04:32:20 : Search time 484 Seconds

(without alignments)
5673.251 Million cell updates/sec

Title: US-10-726-422-1

Perfect score: 412

Sequence: 1 TATCAGCTAGGGCTGGACCC.....AAATGTTTTCACAGCTCT 412

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332246308 residues

Total number of hits satisfying chosen parameters:

4583304

Minimum DB seq length: 10

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s;*  
2: Geneseqn1990s;*  
3: Geneseqn2000s;*  
4: Geneseqn2001as;*  
5: Geneseqn2001bs;*  
6: Geneseqn2002as;*  
7: Geneseqn2002bs;*  
8: Geneseqn2003as;*  
9: Geneseqn2003bs;*  
10: Geneseqn2003cc;*  
11: Geneseqn2003dd;*  
12: Geneseqn2004aa;*  
13: Geneseqn2004bb;*  
14: Geneseqn2005s;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
c 1	24	5.8	2 AAT98004	Aat98004 Human thy
c 2	24	5.8	2 AAT98003	Aat98003 Human thy
c 3	24	5.8	2 APV05152	APV05152 Human thy
c 4	24	5.8	2 APV05151	APV05151 Human thy
c 5	24	5.8	2 APV34009	APV34009 Rat thymo
c 6	24	5.8	2 APV34008	APV34008 Rat thymo
c 7	24	5.8	2 APV15084	APV15084 Human thy
c 8	24	5.8	2 APV15085	APV15085 Human thy
c 9	24	5.8	3 APZ86879	APZ86879 PCR prime
c 10	24	5.8	3 APZ86880	APZ86880 PCR prime
c 11	24	5.8	6 AAD23794	AAD23794 Rat prost
c 12	24	5.8	6 AAD23793	AAD23793 Rat prost
c 13	24	5.8	12 ADF61760	ADF61760 Rat thymo
c 14	24	5.8	12 ADF61759	ADF61759 Rat thymo
c 15	24	5.8	24 12 ADP4492	ADP4492 Human thy
c 16	24	5.8	24 12 ADP4493	ADP4493 Human thy
c 17	21.2	5.8	40 3 Aaa26596	Aaa26596 Human HPC
c 18	20.4	5.0	36 10 ADC02914	ADC02914 Ex vivo
c 19	20.4	5.0	36 12 AD158589	AD158589 Human int

ALIGNMENTS

c 20	20.2	4.9	25 6 ABS52117	Human but
c 21	19.6	4.8	35 3 AAC63164	Minisat
c 22	19.6	4.8	40 6 ABL35224	Immunost
c 23	19.4	4.7	33 10 ADC36204	Wet cont
c 24	19.4	4.7	39 14 ADZ71344	Novel cys
c 25	19.4	4.7	40 6 ABK92323	E. coli D
c 26	19.2	4.7	33 2 AAX81507	Primer us
c 27	19	4.6	36 10 ADC02924	Ex vivo
c 28	19	4.6	36 12 AD158599	Human int
c 29	18.8	4.6	36 10 ADC02926	Ex vivo
c 30	18.8	4.6	36 10 ADC02918	Ex vivo
c 31	18.8	4.6	36 10 ADC02916	PCR prime
c 32	18.8	4.6	36 10 ADC02920	Ex vivo
c 33	18.8	4.6	36 12 AD158601	Human int
c 34	18.8	4.6	36 12 AD158591	Human int
c 35	18.8	4.6	36 12 AD158593	Human int
c 36	18.8	4.6	36 12 AD158595	Human int
c 37	18.6	4.5	31 2 AAX61214	
c 38	18.6	4.5	31 2 ABQ74074	Microsat
c 39	18.6	4.5	33 6 ABN86761	Bukaryot
c 40	18.4	4.5	39 4 AAH84339	Human cel
c 41	18.4	4.5	40 6 ABL91386	Chlamydia
c 42	18.2	4.4	39 2 AAT02551	HEK5 extr
c 43	18.2	4.4	40 2 AAT70788	Stenotic
c 44	18	4.4	27 10 ADC02891	Ex vivo
c 45	18	4.4	27 10 ADC03071	Ex vivo

RESULT

1 AAT98004/c

ID AAT98004 standard; cDNA; 24 BP.

XX

AC AAT98004;

XX

DT 10-MAR-1998 (first entry)

XX

DB Human thymosin beta-15 reverse primer T-beta 15.

XX

KW Human; thymosin beta 15; G-actin; cell motility; adenocarcinoma; **BB**; metastasis; PCR; amplification; primer; detection; diagnosis; cancer.

XX

Synthetic.

OS Homo sapiens.

XX

PN US5663071-A.

XX

PD 02-SEBP-1997.

XX

PP 17-JUN-1996; 96US-00664856.

XX

PR 17-JUN-1996; 96US-00664856.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX

PI Zetter BR, Bao L;

XX

DR WPI; 1997-447933/41.

XX

PT DNA encoding thymosin beta-15 - which binds G-actin and regulates cell motility, useful for detecting cancers in e.g. prostate, lung tissues, especially metastatic cancers.

XX

PP Example; Col 12; 22pp; English.

XX

CC Primers AAT98003-T8008 are used to PCR amplify the nucleotide sequence encoding a human thymosin beta-15, a novel protein that binds and sequesters G-actin and also regulates cell motility in e.g. prostate, lung tissues, carcinoma cells. The sequence was isolated from a cDNA library constructed from polyA RNA purified from a highly metastatic cell line AT3.1 derived from Dunning R3327 rat prostatic adenocarcinoma cells. The

CC

CC nucleic acid and proteins can be used to detect increased expression of
 CC the thymosin beta 15 gene in non-testicular cells which has a high
 CC correlation to cancers, e.g. prostate, lung, melanoma and breast cancers,
 CC especially metastatic cancers

XX Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
 XX Query Match 5.8%; Score 24; DB 2; Length 24;
 XX Best Local Similarity 100.0%; Pred. No 6.6e+03;
 XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX OS Synthetic.
 XX Homo sapiens.

XX Db 24 ACCCTGACTGAAAGTCAGCTT 379

XX 24 ACCCTGACTGAAAGTCAGCTT 1

XX RESULT 2
 XX AAT98003 ID AAT98003 standard; cDNA; 24 BP.
 XX AC AAT98003;
 XX DT 10-MAR-1998 (first entry)
 XX DE Human thymosin beta 15 forward primer T-beta 15.
 XX KW Human: thymosin beta 15; G-actin; cell motility; adenocarcinoma; 68;
 XX KW metastasis; PCR; amplification; primer; detection; diagnosis; cancer.
 XX OS Synthetic.
 XX OS Homo sapiens.

XX PN US5663071-A.

XX PD 02-SEP-1997.

XX PP 17-JUN-1996; 96US-00664856.

XX PR 17-JUN-1996; 96US-00664856.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Zetter BR, Bao L;

XX DR WPI: 1997-447933/41.

XX PT DNA encoding thymosin beta-15 - which binds G-actin and regulates cell motility, useful for detecting cancers in e.g. prostate, lung tissues, especially metastatic cancers.
 XX PS Example: Col 12; 22pp; English.
 XX CC Primers AAT98003-#98008 are used to PCR amplify the nucleotide sequence encoding a human thymosin beta-15, a novel protein that binds and sequesters G-actin and also regulates cell motility in prostatic carcinoma cells. The sequence was isolated from a cDNA library constructed from polyA RNA purified from a highly metastatic cell line AT3.1 derived from Dunning R3327 rat prostatic adenocarcinoma cells. The thymosin beta 15 gene in non-testicular cells which has a high correlation to cancers, e.g. prostate, lung, melanoma and breast cancers, especially metastatic cancers

XX SQ Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 XX Query Match 5.8%; Score 24; DB 2; Length 24;
 XX Best Local Similarity 100.0%; Pred. No 6.6e+03;
 XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX OS Synthetic.
 XX Db 1 TATCAGCTAAGTCAGCTGCACTGGCG 24
 XX 1 TATCAGCTAAGTCAGCTGCACTGGCG 24

XX RESULT 3
 XX AAV05152/c ID AAV05152 standard; cDNA; 24 BP.
 XX AC AAV05152;
 XX DT 24-JUN-1998 (first entry)
 XX DE Human thymosin beta-15 PCR primer.
 XX KW antibody; cancer; diagnosis; prognosis; prostate; lung; melanoma; breast;
 XX ss; PCR; primer; amplification.
 XX OS Synthetic.

XX Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
 XX Query Match 5.8%; Score 24; DB 2; Length 24;
 XX Best Local Similarity 100.0%; Pred. No 6.6e+03;
 XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX OS Synthetic.
 XX Homo sapiens.

XX PN WO9748982-A1.

XX PD 24-DEC-1997.

XX PR 13-JUN-1997; 97MO-US010306.

XX PR 17-JUN-1996; 96US-00664857.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Zetter BR, Bao L;

XX DR WPI: 1998-120303/11.

XX PT Diagnosis and prognosis of cancer - by measuring levels of thymosin beta 15 in a biological sample.

XX PT Disclosure: Page 18; 41pp; English.

XX PS Thymosin beta 15 primers AAV05151 and AAV05152 are used for the amplification of thymosin beta 15 gene. Human thymosin beta 15 has the ability to bind and sequester G-actin like other members of the thymosin beta family, it also directly regulates cell motility in prostatic carcinoma cells. Thymosin beta 15 can be detected in bodily fluids using antibodies, PCR primers and probes. A correlation between expression of human thymosin beta 15 and disease state in a number of cancers has been demonstrated. This can be used for the diagnosis and prognosis of prostate, lung, melanoma or breast cancer

XX SQ Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

XX PT Best Local Similarity 100.0%; Pred. No. 6.6e+03;

XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OS Synthetic.

XX Db 356 ACCCTGACTGAAAGTCAGCTGATT 379

XX 24 ACCCTGACTGAAAGTCAGCTGATT 1

XX RESULT 4
 XX AAV05151 ID AAV05151 standard; cDNA; 24 BP.

XX AC AAV05151;

XX DT 24-JUN-1998 (first entry)

XX DE Human thymosin beta-15 PCR primer.

XX KW antibody; cancer; diagnosis; prognosis; prostate; lung; melanoma; breast;

XX ss; PCR; primer; amplification.

XX OS Synthetic.

DE	Human thymosin beta 15 PCR reverse primer SEQ ID NO:9.									
Query Match	Score 24; DB 2; Length 24;									
Best Local Similarity	5.8%; Pred. No. 6.6e+03; Mismatches 0; Indels 0; Gaps 0;									
Matches 24; Conservative	Human; thymosin beta 15; G-actin; cell motility; regulation; prostatic carcinoma; PCR primer; ss.									
By	Synthetic.									
Db	Homo sapiens.									
RESULT 7										
DE	AAV15084 standard; DNA; 24 BP.									
AAV15084;	14-FEB-1997;									
AAV15084;	97US-00801796.									
AAV15084;	20-MAY-1998 (first entry)									
DE	Human thymosin beta 15 PCR forward primer SEQ ID NO:8.									
AAV15084;	Human; thymosin beta 15; G-actin; cell motility; regulation; prostatic carcinoma; PCR primer; ss.									
AAV15084;	Synthetic.									
AAV15084;	Homo sapiens.									
AAV15084;	US5721337-A.									
AAV15084;	24-FEB-1998.									
AAV15084;	14-FEB-1997;									
AAV15084;	97US-00801796.									
AAV15084;	17-JUN-1996;									
AAV15084;	96US-00664856.									
AAV15084;	(CHIL-) CHILDRENS MEDICAL CENT.									
AAV15084;	Human thymosin beta-15 - regulating prostatic carcinoma cell motility.									
AAV15084;	Synthetic.									
AAV15084;	Homo sapiens.									
AAV15084;	XX									
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AAV15084;	XX									

PI Bao L, Zetter BR;
 XX WPI: 2000-136675/12.
 PT Inhibiting thymosin beta 15 expression, useful for diagnosing and
 PT treating cancer.
 XX Example; Col 12; 22pp; English.
 XX This sequence represents a PCR primer for DNA encoding the human thymosin
 CC beta15 protein. The invention relates to a method for inhibiting thymosin
 CC beta15 expression in a cell comprising administering an antibody or
 CC antibody fragment. The method is useful for treating and diagnosing
 CC cancer, particularly prostate cancer.
 XX Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 SQ Query Match 5.8%; Score 24; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT
 YY 1 TATCAGCTAGGGCTCACCGCG 24
 Db 1 TATCAGCTAGGGCTCACCGCG 24

RESULT 10
 AAZ86880/C
 ID AAZ86880 standard; cDNA; 24 BP.
 XX AC AAZ86880;
 XX DT 03-MAY-2000 (first entry)
 XX DE PCR primer for human thymosin betails coding sequence.
 XX KW Thymosin betails; human; expression inhibitor; antibody; diagnosis;
 KW cancer; prostate cancer; therapy; PCR primer; ss.
 XX Homo sapiens.
 XX US6017717-A.
 XX PD 25-JAN-2000.
 XX PF 29-APR-1998; 98US-00069484.
 XX PR 14-FEB-1997; 97US-00801796.
 PR 17-SEP-1997; 97US-00931877.
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX DE Bao L, Zetter BR;
 XX KW Thymosin betails; human; expression inhibitor; antibody; diagnosis;
 KW cancer; prostate cancer; therapy; PCR primer; ss.
 XX Homo sapiens.
 XX US6017717-A.
 XX PD 25-JAN-2000.
 XX PF 29-APR-1998; 98US-00069484.
 XX PR 14-FEB-1997; 97US-00801796.
 PR 17-SEP-1997; 97US-00931877.
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX Bao L, Zetter BR;
 XX WPI: 2000-136675/12.
 PT Inhibiting thymosin beta 15 expression, useful for diagnosing and
 PT treating cancer.
 XX Example; Col 12; 22pp; English.
 XX This sequence represents a PCR primer for DNA encoding the human thymosin
 CC beta15 protein. The invention relates to a method for inhibiting thymosin
 CC beta15 expression in a cell comprising administering an antibody or
 CC antibody fragment. The method is useful for treating and diagnosing
 CC cancer, particularly prostate cancer.
 XX Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
 SQ Query Match 5.8%; Score 24; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT
 YY 356 ACCCTGACTGAAAGTCAGCATTT 379
 Db 24 ACCCTGACTGAAAGTCAGCATTT 1

RESULT 11
 AAD23794/C
 ID AAD23794 standard; DNA; 24 BP.
 XX AC AAD23794;
 XX DT 07-MAR-2002 (first entry)
 DE Rat prostatic adenocarcinoma cell cDNA amplifying tbeta15 reverse primer.
 XX Rat; thymosin betails protein; G-actin; cell motility; therapy;
 KW prostate cancer; cytosstatic; reverse transcription; RT; PCR primer; ss.
 XX OS Rattus sp.
 XX PN US6300479-B1.
 XX PD 09-OCT-2001.
 XX PF 06-AUG-1999; 99US-0036944.
 XX PR 17-JUN-1996; 96US-00664856.
 PR 14-FEB-1997; 97US-00801796.
 PR 17-SEP-1997; 97US-00931877.
 PR 29-APR-1998; 98US-00069484.
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX PI Zetter BR, Bao L;
 XX DR WPI: 2002-033180/04.
 XX An antibody which selectively binds to a thymosin betails protein is
 PT useful to detect, prevent or treat cancer, particularly of the prostate.
 XX Example; Col 12; 22pp; English.
 XX PS
 XX The invention relates to nucleic acids encoding human thymosin betails
 CC protein, that has the ability to bind and sequester G-actin and directly
 CC regulates cell motility in prostatic carcinoma cells. The antibodies of
 CC thymosin betails protein may be used to diagnose, treat or prevent cancer
 CC particularly prostate cancer. The present sequence is a reverse
 CC transcription (RT)-PCR primer used to amplify rat prostatic
 CC adenocarcinoma cell cDNA. This sequence is used in the exemplification of
 CC the invention
 XX Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
 SQ Query Match 5.8%; Score 24; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT
 YY 356 ACCCTGACTGAAAGTCAGCATTT 379
 Db 24 ACCCTGACTGAAAGTCAGCATTT 1

RESULT 12
 AAD23793
 ID AAD23793 standard; DNA; 24 BP.
 XX AC AAD23793;
 XX DT 07-MAR-2002 (first entry)
 DE Rat prostatic adenocarcinoma cell cDNA amplifying tbeta15 forward primer.
 XX KW Rat; thymosin betails protein; G-actin; cell motility; therapy;

KW prostate cancer; cytostatic; reverse transcription; RT; PCR primer; ss.
 XX Rattus sp.
 OS XX US6300479-B1.
 PN XX 09-OCT-2001.
 PD XX 06-AUG-1999; 99US-00369744.
 FF XX 17-JUN-1997; 96US-00664856.
 PR XX 14-FEB-1997; 97US-00801796.
 PR XX 17-SEP-1997; 97US-00931877.
 PR XX 29-APR-1998; 98US-00069484.
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PA PI Zetter BR, Bao L;
 XX DR WPI; 2004-040942/04.
 PR XX An antibody which selectively binds to a thymosin beta15 protein is useful to detect, prevent or treat cancer, particularly of the prostate.
 PT XX Example; Col 12; 22pp; English.
 CC The invention relates to nucleic acids encoding human thymosin beta15 protein, that has the ability to bind and sequester G-actin and directly regulates cell motility in prostatic carcinoma cells. The antibodies of thymosin beta15 protein may be used to diagnose, treat or prevent cancer particularly prostate cancer. The present sequence is a reverse transcription (RT)-PCR primer used to amplify rat prostatic adenocarcinoma cell cDNA. This sequence is used in the exemplification of the invention
 XX Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 SQ Query Match 5.8%; Score 24; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TATCAGCTAGGGCTGACCCGCG 24
 Db 1 TATCAGCTAGGGCTGACCCGCG 24

RESULT 13
 ADF61760_C
 ID ADF61760 Standard; DNA; 24 BP.
 XX AC ADF61760;
 XX DT 12-FEB-2004 (revised)
 DT 29-JAN-2004 (first entry)
 DE Rat thymosin beta-15 RT-PCR primer, SEQ ID NO:9.
 XX Human; rat; thymosin beta-15; G-actin sequestration; cell motility regulation; neoplastic cell; prostatic carcinoma; prostate cancer; lung cancer; melanoma; breast cancer; metastatic cancer; diagnosis; prognosis; antisense therapy; gene therapy; cytosatic; thymosin beta-15 antagonist; adenocarcinoma RNA; reverse transcription-PCR; RT-PCR; Primer; ss.
 OS XX US2002183496-A1.
 PN XX 05-DEC-2002.
 PD XX 05-JUN-2001; 2001US-00874736.
 PR XX 17-JUN-1996; 96US-00664856.

PR 14-FEB-1997; 97US-00801796.
 PR 17-SEP-1997; 97US-0031877.
 PR 29-APR-1998; 98US-00069484.
 PR 06-AUG-1999; 99US-00069744.
 XX PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX PI Zetter BR, Bao L;
 XX DR WPI; 2004-040942/04.
 PR XX New isolated polynucleotide encoding human thymosin betas for diagnosing and prognosing particular cancers, especially metastatic cancers.
 PT XX Example; SEQ ID NO: 9; 23pp; English.
 XX CC The invention relates to human thymosin beta-15 (ADDF61753) and cDNA encoding it (ADDF61752). The invention also relates to recombinant vectors and host cells comprising human thymosin beta-15 nucleic acids, antibodies which specifically bind human thymosin beta-15, oligonucleotides at least 10 nucleotides in length which hybridise to human thymosin beta-15 cDNA, and methods of treating neoplastic cells expressing thymosin beta-15. Like other members of the thymosin beta family, thymosin beta-15 has the ability to bind and sequester G-actin, but unlike other beta thymosins, it also directly regulates cell motility in prostatic carcinoma cells. Additionally, enhanced expression of thymosin beta-15 in non-testicular cells has a high correlation to disease state in a number of cancers such as prostate, lung, melanoma and breast cancer, particularly metastatic cancers. Human thymosin beta-15 nucleic acids can therefore be used in the diagnosis and prognosis of various cancers, especially metastatic cancers. Cancers which express thymosin beta-15 may be treated by suppressing the activity or expression of thymosin beta-15, for example by administering thymosin beta-15 antisense oligonucleotides or thymosin beta-15 specific antibodies. The present sequence is related to the invention.
 XX SQ Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
 SQ Query Match 5.8%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 356 ACCCTGACTGAAAGTCAAGCATT 379
 Db 24 ACCCTGACTGAAAGTCAAGCATT 1

RESULT 14
 ADF61759
 ID ADF61759 standard; DNA; 24 BP.
 XX AC ADF61759;
 XX DT 12-FEB-2004 (revised)
 DT 29-JAN-2004 (first entry)
 DE Rat thymosin beta-15 RT-PCR primer, SEQ ID NO:8.
 XX Human; rat; thymosin beta-15; G-actin sequestration; cell motility regulation; neoplastic cell; prostatic carcinoma; prostate cancer; lung cancer; melanoma; breast cancer; metastatic cancer; diagnosis; prognosis; antisense therapy; gene therapy; cytosatic; thymosin beta-15 antagonist; adenocarcinoma RNA; reverse transcription-PCR; RT-PCR; Primer; ss.
 OS XX Rattus sp.
 PN XX US2002183496-A1.
 PD XX 05-DEC-2002.
 PR XX 05-JUN-2001; 2001US-00874736.
 PR XX 17-JUN-1996; 96US-00664856.

PR 17-JUN-1996; 96US-00664856.
 PR 14-FEB-1997; 97US-00801796.
 PR 17-SEP-1997; 97US-00931877.
 PR 29-APR-1998; 98US-00063484.
 PR 06-AUG-1998; 98US-00369744.
 XX
 (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Zetter BR, Bao L;
 XX
 DR WPI; 2004-459889/43.
 XX
 PR Novel isolated and purified human thymosin betal5, useful for diagnosing
 PT cancers such as prostate, lung, melanoma and breast cancer, particularly
 PT metastatic cancers.
 XX
 PS Example; SEQ ID NO 8; 23pp; English.
 XX
 CC The invention relates to the human thymosin beta-15 polypeptide and the
 CC polynucleotide encoding it. The invention also relates to an antibody
 CC that selectively binds human thymosin beta-15 and a method of treating a
 CC neoplastic cell expressing human thymosin beta-15 by administering to the
 CC cell a compound which suppresses the activity or production of human
 CC thymosin beta-15. The antibody is useful for treating a neoplastic cell
 CC expressing human thymosin beta-15. The polypeptide and antibody are
 CC useful for treating, diagnosing or preventing cancers such as prostate
 CC cancer, lung cancer, melanoma and breast cancer, particularly metastatic
 CC cancers, where enhanced transcripts (mRNA) and expression of the thymosin
 CC beta-15 gene in non-testicular cells have a high correlation to disease
 CC state in the cancers. (II) is useful for treating or preventing cancers.
 CC This sequence represents a reverse transcriptase PCR (RT-PCR) primer used
 CC to amplify cDNA encoding the human thymosin beta-15 polypeptide of the
 CC invention.
 XX
 SQ Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 5.8%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB
 Qy 1 TATCAGCTAGGGCTGACCCGGCG 24
 Db 1 TATCAGCTAGGGCTGACCCGGCG 24
 XX
 SQ Sequence 24 BP; 4 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 5.8%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 TATCAGCTAGGGCTGACCCGGCG 24
 Db 1 TATCAGCTAGGGCTGACCCGGCG 24
 XX
 RESULT 15
 ADP44092
 ID ADP44092 standard; DNA; 24 BP.
 XX
 AC ADP44092;
 XX
 DT 12-AUG-2004 (First entry)
 XX
 DE Human thymosin beta-15 cDNA RT-PCR primer #1.
 XX
 KW Human; thymosin beta-15; RT-PCR; ss; cancer; prostate; lung; melanoma;
 KW breast; cytosolic; primer; reverse transcriptase.
 XX
 OS Homo sapiens.
 XX
 PN US20041010-A1.
 XX
 PD 27-MAY-2004.
 XX
 PP 03-DEC-2003; 2003US-00726422.
 XX
 PR 17-JUN-1996; 96US-00664856.
 PR 14-FEB-1997; 97US-00801796.
 PR 17-SEP-1997; 97US-00931877.
 PR 29-APR-1998; 98US-00063484.

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Copyright (c) 1993 - 2006 Biocceleration Ltd.	AU254837	AU254837		
OM nucleic - nucleic search, using sw model	BH901287	BH901287		
Run on: March 12, 2006, 05:37:06 ; Search time 3628 Seconds	CF301054	CF301054		
(without alignments)	AJ595967	AJ595967		
5313.197 Million cell updates/sec	Arabidopsis	Arabidopsis		
Title: US-10-726-422-1	CG725443	CG725443		
Perfect Score: 412	C47533	C47533		
Sequence: 1 TATCAGCTAGTGCTGCCACC.....AAATGTTTTCCACGTCTC 412	BH846339	BH846339		
Scoring table: IDENTITY_NUC	AZ312621	AZ312621		
Gapop 10.0 , Gapext 1.0	IM0028C18	IM0028C18		
Searched: 41078325 seqs, 2333541228 residues	CL528781	CL528781		
Total number of hits satisfying chosen parameters: 105260	HIV69909.	HIV69909.		
Minimum DB seq length: 10	A947987	A947987		
Maximum DB seq length: 40	og5860.s	og5860.s		
Post-processing: Minimum Match 0%	CZ466979	CZ466979		
Maximum Match 100%	C012043P	C012043P		
Lassing first 45 summaries	AW46552	AW46552		
RESULT 1	AW6401.X	AW6401.X		
CR399055/c	AJ958580	AJ958580		
LOCUS	BZ290649	BZ290649		
DEFINITION	SALK_0508	SALK_0508		
Arabidopsis thaliana T-DNA flanking sequence GK_8114P03-025642,				
genomic survey sequence.				
CR399055				
ACCESSION				
VERSION				
CR399055..1				
GSS				
Arabidopsis thaliana				
Arabidopsis thaliana				
Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
Spermatophyta; Magnoliophyta; eudicots; core eudicots; ledans;				
rosids; eurosids II; Brassicaeae; Brassicaceae; Arabidopsis.				
REFERENCE				
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.				
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for				
the identification of T-DNA insertion mutants in Arabidopsis				
thaliana				
Bioinformatics 19 (11), 1441-1442 (2003)				
JOURNAL				
PUBMED				
12874060				
REFERENCE				
2				
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and				
Weisshaar, B.				
Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for				
flanking sequence tag-based reverse genetics				
Plant Mol. Biol. 53 (1-2), 247-259 (2003)				
COMMENT				
3				
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and				
Weisshaar, B.				
High-throughput generation of sequence indexes from T-DNA				
mutagenized Arabidopsis thaliana lines				
Bioinformatics 35 (6), 1164-1168 (2003)				
4				
(bases 1 to 36)				
Strizhov, N., Li, Y., Rosso, M.G. and Weisshaar, B.				
Direct Submission				
JOURNAL				
Submitted (01-MAY-2004) Weisshaar, B., Max-Planck-Institut fuer				
Zuechtungsforschung, Carl-von-Linne-weg 10, Koeln, 50829, Germany				
This sequence has been recovered from the left border of the T-DNA.				
It indicates an insertion close to or within gene At1g08790.				
Details on the protocols used for generation of the sequence are				
described in References 1-3. The sequences are generated at the MPI				
for Plant Breeding Research in the context of the GABI-Kat project.				
GABI-Kat is part of the German Plant Genomics program designated				
Result	Query	Description		
No.	Score	Match Length	DB	ID
-----	-----	-----	-----	-----
c 1	19.4	4.7	CR399055	CR399055 Arabidopsis
c 2	19	4.6	9	BH812364 SALK_0616
c 3	18.8	4.6	39	AW247125 2819775..3
c 4	18.6	4.5	33	AZ311457 IM0026121
c 5	18.6	4.5	39	C2914406 4013006 G1
c 6	18.2	4.4	35	AZ450518 IM0249J13
c 7	18	4.4	37	AL952209 Arabidopsis
c 8	18	4.4	39	CZ467113 C01377..5P
c 9	18	4.4	40	AI185980 q834c06..8
c 10	17.8	4.3	31	AA912393 o199c01..8
c 11	17.8	4.3	37	AI181597 uc63d11..r
c 12	17.6	4.3	38	CZ493039 F07653..3P
c 13	17.6	4.3	38	AJ593144 Arabidopsis
c 14	17.4	4.2	36	D19985 HUNGS00952
c 15	17.4	4.2	39	AB088497 AB088497
c 16	17.2	4.2	34	AA624893 vn83h01..r
c 17	17.2	4.2	36	D21040 HUNGS02024
c 18	17.2	4.2	38	BW593140 BW593140
c 19	17.2	4.2	40	B228840 SALK_0219
c 20	17	4.1	34	BJ666456 BJ066456
c 21	17	4.1	36	AJ600605 Arabidopsis
c 22	17	4.1	39	C0777934 BL0028_H1

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Query

Result No.

Score

Match Length

DB

ID

Description

'GABI', Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES	Source	Query Match	Best Local Similarity	Score	DB	Length	Match
Location/Qualifiers			25;	Conservative	4.6%	9;	DB 9;
1. :38			Matches	0;	Pred. No.	2.5e+06;	Length 36;
/organism="Arabidopsis thaliana"					0;	Gaps	0;
/mol_type="genomic DNA"							
/db_xref="taxon:3702"							
/clone="IGK-814F03-025642"							
/clone lib="Arabidopsis thaliana T-DNA insertion lines"							
/ectotype="Col-0"							
/note="PCR was performed on DNA from Arabidopsis thaliana plants (M1) which were transformed with the T-DNA from vector pAC106 (GenBank accession number: AJ57513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."							
ORIGIN							
Query Match		4.7%	Score 19.4;	DB 11;	Length 38;		
Best Local Similarity		70.3%	Pred. No.	2e+06;			
Matches		26;	Conservative	0;	Mismatches	11;	Indels 0;
Qy		101	AGTGATAAACAGAACATTATCGAAGTGTGAAACATTG	137			
Db		38	AGCGAAAGTCAGATCTGAAATGAAATTATTG	2			
RESULTS							
BH812364/C		BH812364	36 bp	DNA	linear	GSS 02-MAY-2002	
LOCUS							
DEFINITION		Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_061675, genomic survey sequence.					
ACCESSION		BH812364					
VERSION		061675					
KEYWORDS							
SOURCE							
ORGANISM							
Arabidopsis thaliana (thale cress)							
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicotyledons; Rosids; euroids II; Brassicales; Brassicaceae; Arabidopsis.							
REFERENCE			1 (bases 1 to 36)				
AUTHORS		Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinbar, C., Jeske, A., Karnes, M., Kim, C.U., Parker, H., Prednis, L., Shin, P., Zimmerman, J., and Ecker, J.R.					
TITLE		A Sequence-indexed Library of Insertion Mutations in the Arabidopsis Genome					
JOURNAL		Unpublished (2001)					
COMMENT		Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu					
CLASS		TDNA tagged.					
FEATURES	Location/Qualifiers	1. :36	/organism="Arabidopsis thaliana"		Site 1: Xhol; Site 2:		
Source			/mol_type="genomic DNA"		/note="Organ: lung; Vector: pONT7; Site 1: Xhol; Site 2: EcoRI; cDNA made by oligo-dT priming, Directionally cloned into BcRI/XhoI sites using the following 5'		
			/ectotype="Col-0"		/adaptor: GGCACGAG (G). Size-selected >50bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		
			/db_xref="taxon:3702"				
			/clone="SALK_061675"				
			/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"				
			TDNA insertion lines				
			each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tDNA_protocols.html "				
ORIGIN							
Query Match		4.6%	Score 18.8;	DB 1;	Length 39;		
Best Local Similarity		68.4%	Pred. No.	2.9e+06;			
Matches		26;	Conservative	0;	Mismatches	12;	Indels 0;

Y	140	AAATCAAAGTGAAGAGACTAATCTGAAAGAAA	177	Qy	150	TGAAAGAGACTAATCTGAGAAA	174
Y	38	AAAGAAAGAAATAAAGAAATAAAGAAATAAAGAAA	1	Db	30	TAAGATGATAATTCTGAGAAA	6
RESULT 4	12311457/c						
LOCUS	AZ311457	33 bp	DNA	linear	GSS 29-SEP-2000		
DEFINITION	1M002611R	Mouse 10kb plasmid UGCC1M library Mus musculus genomic					
CLONE	UGCC1M002611 R	genomic survey sequence					
ACCESSION	AZ311457						
VERSION	AZ311457.1						
ORGANISM	Mus musculus	(house mouse)					
KEYWORDS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognatheti; Muroidea; Muridae; Murinae; Mus.						
REFERENCE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenin, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhäusern, A. and Wright, D., Weiss, R.						
AUTHORS							
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts						
JOURNAL	Unpublished (2000)						
COMMENT	Contact: Robert B. Weiss						
ORGANISM	University of Utah Genome Center						
KEYWORDS	University of Utah						
FEATURES	RM 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA						
source	Tel: 801 585 5606						
source	Fax: 801 585 7177						
source	E-mail: ddunng@genetics.utah.edu						
source	Insert Length: 10000	Std. Error: 0.00					
source	Plate: 0026	Row: I	Column: 21				
source	Seq primer: CACACGAAACAGCTATGACC						
source	Class: plasmid ends						
source	High quality sequence stop: 33						
source	Location/Qualifiers						
source	1..33						
source	/organism="Mus musculus"						
source	/mol_type="Genomic DNA"						
source	/src_train="C57BL/6J"						
source	/db_xref="taxon:10090"						
source	/clone="UGCC1M0026121"						
source	/sex="Male"						
source	/lab_host="E. Coli Strain XL10-Gold, T1-resistant, F-						
source	/clone_id="Mouse 10kb plasmid UGCC1M library"						
source	/note="Vector: PWD22nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnare/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (Gi 4732114 gb AF125072.1), a copy-number inducible derivative of Plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL1-Gold (Stratagene) cells and selected for ampicillin resistance."						
ORIGIN							
RESULT 5	12311457/c						
LOCUS	CZ914406	39 bp	DNA	linear	GSS 08-AUG-2005		
DEFINITION	4013006511.1BL_Y1	4013	-	RescueMu	Grid O	Zea mays	genomic
LOCUS	CZ914406	39 bp	DNA	linear	GSS 08-AUG-2005		
DEFINITION	4013006511.1BL_Y1	4013	-	RescueMu	Grid O	Zea mays	genomic
ACCESSION	CZ914406.1	GI:71930997					
VERSION	CZ914406						
KEYWORDS	Zea mays						
ORGANISM	Zea mays						
REFERENCE	Eukaryota; Viridiplantae; Streptophytai; Embryophytai; Tracheophytai; Spermatophytai; Magnoliophytai; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.						
AUTHORS	1 (bases 1 to 39); Walbot, V.						
TITLE	Maize genomic sequences found using engineered RescueMu transposon						
JOURNAL	Unpublished (2001)						
COMMENT	Contact: Walbot, V.						
ORGANISM	Department of Biological Sciences						
REFERENCE	Stanford University						
AUTHORS	855 California Ave, Palo Alto, CA 94304, USA						
TITLE	Very probable ligation site of ends cut by single endonuclease.						
JOURNAL	Reverse complemented post-ligation sequence from source sequence.						
COMMENT	Plate: 4013006	row: G	column: 11				
ORGANISM	Class: transposon-tagged.						
REFERENCE	Class: transposon-tagged.						
AUTHORS	Location/Qualifiers						
TITLE	1..39						
JOURNAL	/organism="Zea mays"						
COMMENT	/mol_type="genomic DNA"						
ORGANISM	/culc�var="mixed background W23/A188/B73/K55"						
REFERENCE	/db_xref="taxon:4577"						
AUTHORS	/tissue_type="leaf"						
TITLE	/dev_stager="adult"						
JOURNAL	/lab_host="DH10B"						
COMMENT	/clone_idb="0103	-	RescueMu Grid O"				
ORGANISM	/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site ' http://www.mutransposon.org/project/RescueMu/ '. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to the blunt ends of circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."						
ORGANISM	Query Match	4.5%	Score 18.6;	DB 10;	Length 39;		
REFERENCE	Best Local Similarity	72.7%	Pred. No. 3	3e-06;			
AUTHORS	Matches 24;	Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 10;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
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ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
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TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
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ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
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TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
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TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
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AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
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JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
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TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
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REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
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AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
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AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
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TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
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ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
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AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
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TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
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ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
JOURNAL	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
COMMENT	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
ORGANISM	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		
REFERENCE	Best Local Similarity	84.0%	Pred. No. 3	2e-06;			
AUTHORS	Matches 21;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;	
TITLE	Query Match	4.5%	Score 18.6;	DB 9;	Length 33;		

VERSION	AZ450518.1	GI:	10605384	ACCESSION	AL952209
SOURCE	GSS . Mus musculus (house mouse)			KEYWORD	GI:24408831
ORGANISM	Mus musculus			SOURCE	Al952209
REFERENCE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.			ORGANISM	Arabidopsis thaliana (thale cress)
AUTHORS	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			REFERENCE	Arabidopsis; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath; Muridae; Murinae; Mus.
TITLE	Unpublished (2000)			AUTHORS	Arabidopsis thaliana; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
JOURNAL	COMMENT			TITLE	Li, Y., Rosso, M.G., Strizhov, N., Viehöver, P. and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@gentech.utah.edu			JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)
FEATURES	Insert Length: 10000 Std Error: 0.00 Place: 049 row: J column: 13 Seq primer: GTTCTTAAACGACGCCCACT Class: Plasmid ends High quality sequence stop: 35.			PUBLISHED	12874960
FEATURES	Location/Qualifiers			REFERENCE	2
FEATURES	1 .. 35 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:1090" /clone="UUGC1M0249J13" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UGCLM library" /note="Vector: pND420N. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnare/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gil473214 [gb]AF129072.1), a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapter mouse DNA was annealed to adapter vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			AUTHORS	Li, Y., Strizhov, N., Rosso, M.G., Viehöver, P., Dekker, K.A. and Weisshaar, B.
FEATURES	ORIGIN			TITLE	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
FEATURES				JOURNAL	Plant Mol. Biol. 53 (1-2), 241-259 (2003)
FEATURES				PUBLISHED	1475621
FEATURES				REFERENCE	3
FEATURES				AUTHORS	Strizhov, N., Li, Y., Rosso, M.G., Viehöver, P., Dekker, K.A. and Weisshaar, B.
FEATURES				TITLE	High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
FEATURES				JOURNAL	Biotechnology 35 (6), 1164-1168 (2003)
FEATURES				PUBLISHED	14682050
FEATURES				REFERENCE	4 (bases 1 to 37)
FEATURES				AUTHORS	Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.
FEATURES				TITLE	Direct Submission
FEATURES				JOURNAL	Submitted (31-MAR-2004) Weisshaar, B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linné-Weg 10, Koeln, 50839, Germany
COMMENT				COMMENT	This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g06610.
					Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
					Location/Qualifiers
					1 .. 37
					/organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /clone="GK-341F12-016153" /clone_lib="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Col-0"
					/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
					ORIGIN
					Query Match 4.4%; Score 18.2; DB 9; Length 35;
					Best Local Similarity 74.2%; Pred. No. 4.2e+06; Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy	94 CAAGTGTAGTCATAAACCACTATCAGAA 124			Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Db	3 CAAGTAACTGATAATCATGCTATGAGAA 33			QY 283 TGGATTAGACATCTTGTAACCC 308	
				Db 2 TTGATTAAGACATATTGTGTAAC 27	
RESULT	7			RESULT 8	
AL952209	Al952209	37 bp	DNA linear	CZ467113	
LOCUS	Arabidopsis thaliana T-DNA flanking sequence GK-341F12-016153, genomic survey sequence			C2467113	
DEFINITION				DEFINITION 01377-5prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic sequence recovered from 5' end of piggyBac,	

ACCESSION VERSION	CZ67113 CZ67113.1	GI	62861126	IMAGE:1740874 3' similar to TR:Q33574 Q33574 ORF2 BASES 1807-2850. ; mRNA sequence. A1185980
KEYWORDS	GSS.	ACCESSION	EST.	
SOURCE	Drosophila melanogaster (fruit fly)	VERSION	A1185980.1	GI:3736618
ORGANISM	Drosophila melanogaster	KEYWORDS		
REFERENCE		SOURCE	Homo sapiens (human)	
AUTHORS	Nepture; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Euryptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydrioidea; Drosophilidae; Drosophila.	ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
COMMENT	Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Denkay, M., Fawcett, R., Francis-Lang, H.L., Nepture, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L. and Margolis, J.	REFERENCE	1 (bases 1 to 39) NCTI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
JOURNAL	A complementary transposon tool kit for <i>Drosophila melanogaster</i> Nat. Genet. 36 (3), 283-287 (2004)	AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
PUBMED	14981521	TITLE	Unpublished (1997)	
COMMENT	Contact: Roger A. Hoskins Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA Tel: 510 486 4015 Fax: 510 486 6798 Email: RHoskins@lbl.gov	FEATURES	COMMENT /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1740874" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares_fetal_lung_NbHH19W" /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACATCTGAGTGAGGGAGCGCGATTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetus heart NbHH19W."	
FEATURES		LOCATION/QUALIFIERS	ORIGIN	
SOURCE		1. 39 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /strain="isogenic w- strain" /db_xref="taxon:7227" /clone_lib="Exelixis piggyBac PB insertions" /note="Vector: piggyBac PB (GenBank accession number AY515146); An isogenic w- <i>Drosophila melanogaster</i> strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37oC water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homologous viability, and used for recovery of flanking genomic sequence by inverse PCR."	RESULT 10 AA912393 LOCUS DEFINITION	Query Match 4.4%; Score 18; DB 1; Length 40; Best Local Similarity 70.6%; Pred. No. 4.8e+06; Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0; Similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ; mRNA sequence.
SOURCE		ORGANISM	AA912393 EST.	
REFERENCE		ORGANISM	Homo sapiens (human)	
AUTHORS		ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
TITLE		REFERENCE	1 (bases 1 to 31) NCTI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
		AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
		DEFINITION		
RESULT 9 A1185980/C	211 GAAGAGATAATACAAAGATCATATAATGAGATT 244 4 GAAGAGATAATACAAAGATCATATAATGAGATT 37	LOCUS	40 bp mRNA linear EST 29-OCT-1998	
DEFINITION	Scares_fetal_lung_NbHH19W Homo sapiens cDNA clone	DEFINITION		

JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Straubberg, Ph.D. Email: cgsabre@mail.nih.gov
unknown library type	
Insert Length:	720 Std Error: 0.00
Seq Primer:	-40m13 fwd. ET from Amerham
High quality sequence stop:	1.
Location/Qualifiers	1..31
FEATURES	
SOURCE	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1537728" /tissue_type="dorsal root ganglion" /lab_host="DH10B" /clone_lib="DH10B" /note="Organ: Peripheral nervous system; Vector: pCMV-SPORT4; Site: SaliI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb."
ORIGIN	
Query Match	4.3%; Score 17.8; DB 1; Length 31;
Best Local Similarity	75.9%; Pred. No. 5.2e+06;
Matches	22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy	278 AGTCCTGGATTAGACATGGTCGTGTA 306
Db	2 AGCCAGGTACTAACTGGTCGTGTA 30
RESULT 11	
LOCUS	AI181597
DEFINITION	37 bp mRNA Soares mammary gland muscle cDNA clone IMAGE:1430125 5' Similar To SW:CB_HUMAN Q9828 SNK INTERACTING PROTEIN 2-28 ; mRNA sequence.
ACCESSION	AI181597
VERSION	AI181597.1
KEYWORDS	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	1 (bases 1 to 37)
AUTHORS	Mariotti,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Sciumoonath,M., Muroideas; Murinae; Murinae; Mus.
TITLE	The WashU-HMMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; Contact the IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES	
SOURCE	MGI:914393 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090"
ORIGIN	
Query Match	4.3%; Score 17.8; DB 1; Length 37;
Best Local Similarity	67.6%; Pred. No. 5.4e+06;
Matches	25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy	41 GGACTAGCTGGCACAGATTGCTGGCTAGTAAAG 77
Db	1 GCAGTCGTGTCTAAGGACTGTCAGTACAG 37
RESULT 12	
LOCUS	CZ490399
DEFINITION	38 bp DNA linear GSS 29-APR-2005 piggyBac WH insertions Drosophila melanogaster genomic sequence recovered from 3' end of piggyBac, genomic survey sequence.
ACCESSION	CZ490399
VERSION	F07663-3 prime
KEYWORDS	Exelixis piggyBac WH insertions Drosophila melanogaster genomic survey sequence.
SOURCE	CZ490399.1
ORGANISM	GSS
REFERENCE	Thibault,S.T., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L., Singh,C.M., Cheung,L.M., Chong,A., Erickson,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Greer,K., Hartoni,S.R., Howie,E., Jakkula,L., Joo,D., Killback,K., Laufer,A., Mazzotta,J.J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Ventura,R., Woo,A., Zakrzejsek,I., Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L., and Margolis,J.
AUTHORS	A complementary transposon tool for Drosophila melanogaster using P and piggyBac
TITLE	Nat. Genet. 36 (3), 283-287 (2004)
JOURNAL	14981521
PUBLMED	COMMENT
COMMENT	Contact: Roger A Hoskins Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA Tel: 510 486 4015 Fax: 510 486 6798 Email: Rhoskins@lbl.gov
FEATURES	
SOURCE	Sequence recovery method was inverse PCR. Sequence orientation is forward strand relative to 5' end of piggyBac element. The piggyBac insertion position is 1 in the 38 bases. This insertion position refers to the first base of the 4 base TAA target recognition sequence.
QUALIFIERS	Location/Qualifiers
1..37	1. .38 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /strain="isogenic w- strain"

TITLE Small RNAs detected in the rice phloem sap
JOURNAL Unpublished (2003)
COMMENT Contact: Hironorri Mano
 Plant Genome Center Co.,Ltd
 Kanondai-1-25-2, Tsukuba, Ibaraki 305-0856, Japan
 Tel: 81-298-39-4823
 Email: hmano@pgcna.co.jp.
FEATURES
Source Location/Qualifiers
 1. 39
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="PA426"
 /tissue="phloem"
 /clone_Tib="lambda TripleX2 rice phloem sap cDNA"
ORIGIN
 Query Match 4.2%; Score 17.4; DB 1; Length 39;
 Best Local Similarity 77.8%; Fred. No. 7e+06;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 214 AGAATAATCAAGATCATAAATCA 240
Db 5 AATATATCTCATATGATATGATATG 31

Search completed: March 12, 2006, 06:44:17
 Job time : 3632 secs

maximum DB seq length: 40
post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries
RESULT 1

Published Applications NA Main:*

1: /cgr2_6_ptodata/1/pubpna/us07_puccomb.seq:*

2: /cgr2_6_ptodata/1/pubpna/us08_puccomb.seq:*

3: /cgr2_6_ptodata/1/pubpna/us09_puccomb.seq:*

4: /cgr2_6_ptodata/1/pubpna/us09b_puccomb.seq:*

5: /cgr2_6_ptodata/1/pubpna/us10_puccomb.seq:*

6: /cgr2_6_ptodata/1/pubpna/us10b_puccomb.seq:*

7: /cgr2_6_ptodata/1/pubpna/us10c_puccomb.seq:*

8: /cgr2_6_ptodata/1/pubpna/us10d_puccomb.seq:*

9: /cgr2_6_ptodata/1/pubpna/us10e_puccomb.seq:*

10: /cgr2_6_ptodata/1/pubpna/us11_puccomb.seq:*

red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
1	25	6.1	25	7	US-10-719-956-99595	Sequence 99595, A			
2	25	6.1	25	7	US-10-719-956-151661	Sequence 151661,			
3	25	6.1	25	7	US-10-719-956-200130	Sequence 200130,			
4	25	6.1	25	7	US-10-719-956-293879	Sequence 283879,			
5	25	6.1	25	7	US-10-719-956-302980	Sequence 302980,			
6	25	6.1	25	7	US-10-719-956-338333	Sequence 338333,			
7	25	6.1	25	7	US-10-719-956-533192	Sequence 533192,			
8	25	6.1	25	7	US-10-719-956-551423	Sequence 55943,			
9	25	6.1	25	7	US-10-719-956-560901	Sequence 560901,			
10	25	6.1	25	7	US-10-719-956-582115	Sequence 562115,			
11	25	6.1	25	7	US-10-719-956-589182	Sequence 589182,			
12	24	5.8	24	3	US-09-874-736-8	Sequence 8, Appli			
13	24	5.8	24	3	US-09-874-736-9	Sequence 9, Appli			
14	24	5.8	24	7	US-10-726-122-8	Sequence 8, Appli			
c	15	24	5.8	24	7	US-10-726-122-9	Sequence 9, Appli		
c	16	23.4	5.7	25	7	US-10-719-956-99596	Sequence 99596, A		
c	17	23.4	5.7	25	7	US-10-719-956-151662	Sequence 151662,		
c	18	23.4	5.7	25	7	US-10-719-956-200127	Sequence 200127,		
c	19	23.4	5.7	25	7	US-10-719-956-283880	Sequence 283880,		
c	20	23.4	5.7	25	7	US-10-719-956-320981	Sequence 320981,		
c	21	23.4	5.7	25	7	US-10-719-956-338332	Sequence 338332,		
c	22	23.4	5.7	25	7	US-10-719-956-533193	Sequence 533193,		
c	23	23.4	5.7	25	7	US-10-719-956-550422	Sequence 550422,		

ORGANISM: *Rattus norvegicus*
US-10-719-956-151661

Query Match 6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 368 AGTCAGCATTAAACCAATT 392
Db 1 AGTCAGCATTAAACCAATT 25

RESULT 3
US-10-719-956-200130
; Sequence 200130, Application US/10719956
; Publication No. US0040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO: 302980
LENGTH: 25
TYPE: DNA
ORGANISM: *Rattus norvegicus*
US-10-719-956-302980

Query Match 6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 GAAGCTTGGAAACGAGCACTCAAGA 98
Db 1 GAAGCTTGGAAACGAGCACTCAAGA 25

RESULT 6
US-10-719-956-338333
; Sequence 338333, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO: 338333
LENGTH: 25
TYPE: DNA
ORGANISM: *Rattus norvegicus*
US-10-719-956-338333

Query Match 6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 239 GAGATTCTCCCTCTGAAGCAACT 263
Db 1 GAGATTCTCCCTCTGAAGCAACT 25

RESULT 7
US-10-719-956-533192
; Sequence 533192, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO: 533192
LENGTH: 25
TYPE: DNA
ORGANISM: *Rattus norvegicus*
US-10-719-956-283879

Query Match 6.1%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 GAAAGAAATCTCTCTCCAGG 194
Db 1 GAAAGAAATCTCTCTCCAGG 25

RESULT 5
US-10-719-956-302980
; Sequence 302980, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator v 1.1
SEQ ID NO: 533192
LENGTH: 25
TYPE: DNA
ORGANISM: *Rattus norvegicus*

US-10-719-956-5333192
 Query Match 6.1%; Score 25; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03; Mismatches 0;
 Matches 25; Conservative 0; Indels 0; Gaps 0;
 Qy 296 GTTTCGTAAACCTATCCAAATATGT 320
 Db 1 GTTTCGTAAACCTATCCAAATATGT 25
 SEQ ID NO: 699466
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 LENGTH: 25
 RESULT 8
 US-10-719-956-559423
 Sequence 559423, Application US/10719956
 Publication No. US20040146910A1
 GENERAL INFORMATION:
 APPLICANT: Xue Mei Zhou
 TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 FILE REFERENCE: 3527.1
 CURRENT APPLICATION NUMBER: US/10/719,956
 CURRENT FILING DATE: 2003-11-20
 PRIOR APPLICATION NUMBER: 60/427,836
 PRIOR FILING DATE: 2002-11-20
 NUMBER OF SEQ ID NOS: 699466
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 559423
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 US-10-719-956-559423
 Query Match 6.1%; Score 25; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03; Mismatches 0;
 Matches 25; Conservative 0; Indels 0; Gaps 0;
 Qy 45 TAGCTCGGACAGAAATGCTGCCT 69
 Db 1 TAGCTCGGACAGAAATGCTGCCT 25
 SEQ ID NO: 559423
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 LENGTH: 25
 RESULT 9
 US-10-719-956-560901
 Sequence 560901, Application US/10719956
 Publication No. US20040146910A1
 GENERAL INFORMATION:
 APPLICANT: Xue Mei Zhou
 TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 FILE REFERENCE: 3527.1
 CURRENT APPLICATION NUMBER: US/10/719,956
 CURRENT FILING DATE: 2003-11-20
 PRIOR APPLICATION NUMBER: 60/427,836
 PRIOR FILING DATE: 2002-11-20
 NUMBER OF SEQ ID NOS: 699466
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 560901
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 US-10-719-956-560901
 Query Match 6.1%; Score 25; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03; Mismatches 0;
 Matches 25; Conservative 0; Indels 0; Gaps 0;
 Qy 329 TAGGCCTTCTGTAGGGCTTAA 353
 Db 1 TAGGCCTTCTGTAGGGCTTAA 25
 SEQ ID NO: 560901
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 LENGTH: 25
 RESULT 10
 US-10-719-956-562115
 Sequence 562115, Application US/10719956
 Publication No. US20040146910A1
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 US-10-719-956-562115
 Query Match 6.1%; Score 25; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03; Mismatches 0;
 Matches 25; Conservative 0; Indels 0; Gaps 0;
 Qy 343 TAGGTCTTAAGTACCTGACTGAA 367
 Db 1 TAGGTCTTAAGTACCTGACTGAA 25
 SEQ ID NO: 562115
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 LENGTH: 25
 RESULT 11
 US-10-719-956-589182
 Sequence 589182, Application US/10719956
 Publication No. US20040146910A1
 GENERAL INFORMATION:
 APPLICANT: Xue Mei Zhou
 TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 FILE REFERENCE: 3527.1
 CURRENT APPLICATION NUMBER: US/10/719,956
 CURRENT FILING DATE: 2003-11-20
 PRIOR APPLICATION NUMBER: 60/427,836
 PRIOR FILING DATE: 2002-11-20
 NUMBER OF SEQ ID NOS: 699466
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 589182
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 US-10-719-956-589182
 Query Match 6.1%; Score 25; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03; Mismatches 0;
 Matches 25; Conservative 0; Indels 0; Gaps 0;
 Qy 184 TCCCTCGAAGAAACTATCCAGCAG 208
 Db 1 TCCCTCGAAGAAACTATCCAGCAG 25
 SEQ ID NO: 589182
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 LENGTH: 25
 RESULT 12
 US-09-874-736-8
 Sequence 8, Application US/09874736
 Publication No. US20020183496A1
 GENERAL INFORMATION:
 APPLICANT: BRUCE R. ZETTER AND LERE BAO
 TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
 PROTEIN AND USES THEREOF
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESS: DIKES, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 110 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02119
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/874,736
 FILING DATE: 19-NO. US20020183496A1-2001
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/801,796
 FILING DATE: 14-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 46507
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-6400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: <Unknown>
 ORIGINAL SOURCE:
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-09-874-736-9

RESULT 14
 US-10-726-422-8
 Query Match 5.8%; Score 24; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 24; Mismatches 0; Indels 0; Gaps 0;

Query 356 ACCCTGACTGAAAGTCAGCTT 379
 Db 24 ACCCTGACTGAAAGTCAGCTT 1

RESULT 13
 US-09-874-736-9/c
 Sequence 9, Application US/09874736
 Publication No. US20020183496A1
 GENERAL INFORMATION:
 APPLICANT: BRUCE R. ZETTER AND LERE BAO
 TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
 PROTEIN AND USES THEREOF
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02019
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/726,422
 FILING DATE: 03-DEC-2003
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,796
 FILING DATE: 14-FEB-1997
 APPLICATION NUMBER: 08/664,856
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 46507
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

RESULT 13
 US-09-874,736-9/c
 Sequence 9, Application US/09874736
 Publication No. US20020183496A1
 GENERAL INFORMATION:
 APPLICANT: BRUCE R. ZETTER AND LERE BAO
 TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
 PROTEIN AND USES THEREOF
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02019
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/874,736
 FILING DATE: 19-NO. US20020183496A1-2001
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/801,796
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 46507
 TELECOMMUNICATION INFORMATION:

FRAGMENT TYPE: <Unknown>
 ORIGINAL SOURCE: <Unknown>
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-10-726-422-8

Query Match 5.8%; Score 24; DB 7; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 24; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 TATCGCTAGGGCTGACCCGGCG 24
 Db 1 TATCGCTAGGGCTGACCCGGCG 24

RESULT 15

US-10-726-422-9/c

Sequence 9, Application US/10726422
 Publication No. US 0040101910A1
 GENERAL INFORMATION:
 APPLICANT: BRUCE R. ZETTER AND LERE BAO
 TITLE OF INVENTION: HUMAN THYMOSIN 15 GENBNE,
 NUMBER OF SEQUENCES: 13
 PROTEIN AND USES THEREOF

CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02019

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/726,422
 FILING DATE: 03-Dec-2003
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,796
 FILING DATE: 14-FEB-1997
 APPLICATION NUMBER: 08/664,856
 FILING DATE: 17 JUN 1996

ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 46507
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: <Unknown>
 ORIGINAL SOURCE: <Unknown>
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-10-726-422-9

Query Match 5.8%; Score 24; DB 7; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9.6e+03;
 Matches 24; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTCAGCATT 379
 Db 24 ACCCTGACTGAAGGTCAGCATT 1

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OM nucleic - nucleic search, using bw model

Run on: March 12, 2006, 05:58:46 ; Search time 328 Seconds

(without alignments)
2898.190 Million cell updates/sec

Title: US-10-726-422-1

Perfect score: 412

Sequence: 1 TATCAGCTTAGCTGGACCC.....AAATGTTTCACTGCTC 412

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 115348444 residues

Total number of hits satisfying chosen parameters:

1240030308

Minimum DB seq length: 10

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications_NA_New:*

1: /cgnd_6/_ptodata/2/_pubpna/us08 NEW PUB.seq:/*
2: /cgnd_6/_ptodata/2/_pubpna/us06 NEW PUB.seq:/*
3: /cgnd_6/_ptodata/2/_pubpna/us07 NEW PUB.seq:/*
4: /cgnd_6/_ptodata/2/_pubpna/pct_new PUB.seq:/*
5: /cgnd_6/_ptodata/2/_pubpna/us05 NEW PUB.seq:/*
6: /cgnd_6/_ptodata/2/_pubpna/us09 NEW PUB.seq:/*
7: /cgnd_6/_ptodata/2/_pubpna/us10 NEW PUB.seq:/*
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10: /cgnd_6/_ptodata/2/_pubpna/us11 NEW PUB.seq:/*
11: /cgnd_6/_ptodata/2/_pubpna/us11 NEW PUB.seq:/*
12: /cgnd_6/_ptodata/2/_pubpna/us11 NEW PUB.seq:/*
13: /cgnd_6/_ptodata/2/_pubpna/us60 NEW PUB.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.8	5.3	25	12	US-11-121-849-515721
2	20.2	4.9	25	12	US-11-121-849-89187
3	19.4	4.7	25	12	US-11-121-849-884665
C 4	18.6	4.5	25	12	US-11-121-849-240130
C 5	18.2	4.4	25	7	US-10-932-182A-85391
C 6	18.2	4.4	25	12	US-11-121-849-26586
C 7	18.2	4.4	25	19	US-11-101-244-773890
C 8	18	4.4	26	8	US-10-210-914A-1060248
C 9	18	4.4	26	8	US-10-210-914A-1060248
C 10	17.8	4.3	25	12	US-11-121-849-89187
C 11	17.8	4.3	25	12	US-11-121-849-210505
C 12	17.8	4.3	25	12	US-11-121-849-210506
C 13	17.8	4.3	25	12	US-11-121-849-210507
C 14	17.8	4.3	25	12	US-11-121-849-210507
C 15	17.6	4.3	25	7	US-10-932-182A-145807
C 16	17.6	4.3	25	7	US-10-932-182A-145807
C 17	17.6	4.3	25	12	US-11-121-849-46145
C 18	17.6	4.3	25	12	US-11-121-849-50711
C 19	17.6	4.3	25	12	US-11-121-849-239869
C 20	17.6	4.3	25	12	US-11-121-849-301096

RESULT 1		RESULT 2	
US-11-121-849-515721		US-11-113-424-90	
/ Sequence 515721, Application US/11121849		/ Sequence 90, Application US/1113424	
/ Publication No. US20050272080A1		/ Publication No. US2005260713A1	
/ GENERAL INFORMATION:		/ GENERAL INFORMATION:	
/ APPLICANT: John Palma		/ APPLICANT: Gangolfi, et al.	
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St		/ TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same	
/ FILE REFERENCE: 3684.1		/ FILE REFERENCE: 21400-225	
/ CURRENT FILING DATE: 2005-05-03		/ CURRENT FILING DATE: 2005-05-03	
/ PRIOR APPLICATION NUMBER: 60/567,949		/ PRIOR APPLICATION NUMBER: 60/567,949	
/ NUMBER OF SEQ ID NOS: 673304		/ NUMBER OF SEQ ID NOS: 673304	
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1		/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1	
/ SEQ ID NO: 515721		/ SEQ ID NO: 515721	
/ LENGTH: 25		/ LENGTH: 25	
/ TYPE: DNA		/ TYPE: DNA	
/ ORGANISM: Homo sapien		/ ORGANISM: Homo sapien	

ALIGNMENTS		ALIGNMENTS	
c 21	17.6	4.3	25
c 22	17.6	4.3	35
c 23	17.4	4.2	19
c 24	17.4	4.2	19
c 25	17.4	4.2	19
c 26	17.4	4.2	19
c 27	17.4	4.2	19
c 28	17.4	4.2	19
c 29	17.4	4.2	27
c 30	17.4	4.2	36
c 31	17.2	4.2	22
c 32	17.2	4.2	25
c 33	17.2	4.2	25
c 34	17.2	4.2	25
c 35	17.2	4.2	25
c 36	17.2	4.2	25
c 37	17.2	4.2	25
c 38	17.2	4.2	25
c 39	17.2	4.2	25
c 40	17.2	4.2	25
c 41	17.2	4.2	25
c 42	17.2	4.2	30
c 43	17.2	4.2	30
c 44	17	4.1	19
c 45	17	4.1	19

PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; NUMBER OF SEQ ID NOS: 190
; PRIOR FILING DATE: 2001-05-02
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 90
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-11-113-24-90

Query Match 4.9%; Score 20.2%; DB 12; Length 25;
Best Local Similarity 88.0%; Pred. No. 7.4e+04;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 98 ATGAGTGTAAACCGAACATTCAG 122
Db 1 ATGAGTGTAAACCCAACTTGTCAG 25

RESULT 3
US-11-121-849-284665
; Sequence 284665, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 671904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 284665
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-284665

Query Match 4.7%; Score 19.4%; DB 12; Length 25;
Best Local Similarity 95.2%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 292 ACATGTTCTGTAAACCTATC 312
Db 4 ACATGTTCTGTGAACCTATC 24

RESULT 4
US-11-121-849-340130/C
; Sequence 340130, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 89391
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-89391

Query Match 4.5%; Score 18.6%; DB 12; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.8e+05;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 193 GGAAACTTCAGGAGAAAGGA 217
Db 25 GGAAATGATTAGGGGAGAAGGA 1

RESULT 5
US-10-932-182A-89391/C
; Sequence 89391, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: FUJIMURA, YUKIKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 89391
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-89391

Query Match 4.4%; Score 18.2%; DB 7; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.2e+05;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 225 AAAGATCATATAATGAGATTCTC 247
Db 25 AAAGATAATGAAAGAGATTCTC 3

RESULT 6
US-10-932-182A-89391/C
; Sequence 89391, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: FUJIMURA, YUKIKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 89391
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-89391

Query Match 4.4%; Score 18.2; DB 7; Length 25;
 Best Local Similarity 87.0%; Pred. No. 2.2e+05;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 2 AGUCAAGAUGAGUGAUAA 19

RESULT 9
 US-11-083-784-773890
 ; Sequence 773890, Application US/11083784
 ; Publication No. US2005024575A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmaccon, Inc.
 ; APPLICANT: Khrorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13493US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIORITY NUMBER: US/10/714,333
 ; PRIORITY APPLICATION NUMBER: 60/502,050
 ; PRIORITY FILING DATE: 2003-11-14
 ; PRIORITY APPLICATION NUMBER: 60/426,137
 ; PRIORITY FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO: 262586
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-773890

Query Match 4.4%; Score 18.2; DB 11; Length 19;
 Best Local Similarity 77.8%; Pred. No. 2.3e+05;
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 91 AGTCAGATGAGTGTATAA 108
 Db 2 AGUCAAGAUGAGUGAUAA 19

RESULT 10
 US-10-310-914A-1060248
 ; Sequence 1060248, Application US/10310914A
 ; Publication No. US2006003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiles, Kvuzat
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 0087-0200-CPU01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388442
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 1060248
 ; LENGTH: 26
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1060248

Query Match 4.4%; Score 18; DB 8; Length 26;
 Best Local Similarity 73.1%; Pred. No. 2.5e+05;
 Matches 19; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 199 TATCCAGCAGGAGAAAGAATATAATC 224
 Db 1 UAUACGACGAAAPAGAAAPAAAC 26

RESULT 11
 US-11-121-849-89187/C
 ; Sequence 89187, Application US/11121849

Query Match 4.4%; Score 18; DB 10; Length 19;
 Best Local Similarity 77.8%; Pred. No. 2.3e+05;
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 91 AGTCAGATGAGTGTATAA 108
 Db 1 UAUACGACGAAAPAGAAAPAAAC 26

Publication No. US20050272080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John Palma
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Samples
 ; FILE REFERENCE: Microarrays
 ; CURRENT APPLICATION NUMBER: US/11/121,849
 ; FILE REFERENCE: 3684.1
 ; CURRENT FILING DATE: 2005-05-03
 ; PRIOR APPLICATION NUMBER: 60/567,949
 ; PRIOR FILING DATE: 2004-05-03
 ; NUMBER OF SEQ ID NOS: 673904
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO: 69187
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-11-121-849-69187

Query Match 4.3%; Score 17.8; DB 12; Length 25;
 Best Local Similarity 90.5%; Pred. No. 2.8e+05;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 217 ATATAATCAGATCATAAA 237
 Db 23 AGATRATCAGAGCATAAA 3

RESULT 12
 US-11-121-849-210505/C
 ; Sequence 210505, Application US/11121849
 ; Publication No. US20050272080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John Palma
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Samples
 ; FILE REFERENCE: Microarrays
 ; CURRENT APPLICATION NUMBER: US/11/121,849
 ; FILE REFERENCE: 3684.1
 ; CURRENT FILING DATE: 2005-05-03
 ; PRIOR APPLICATION NUMBER: 60/567,949
 ; PRIOR FILING DATE: 2004-05-03
 ; NUMBER OF SEQ ID NOS: 673904
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO: 210505
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-11-121-849-210505

Query Match 4.3%; Score 17.8; DB 12; Length 25;
 Best Local Similarity 90.5%; Pred. No. 2.8e+05;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 144 CAAAGTTGAGAAGCTAATA 164
 Db 24 CAAAGGTGAGAAGCTAATA 4

RESULT 13
 US-11-121-849-210506/C
 ; Sequence 210506, Application US/11121849
 ; Publication No. US20050272080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John Palma
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Samples
 ; FILE REFERENCE: Microarrays
 ; CURRENT APPLICATION NUMBER: US/11/121,849
 ; FILE REFERENCE: 3684.1
 ; CURRENT FILING DATE: 2005-05-03
 ; PRIOR APPLICATION NUMBER: 60/567,949
 ; PRIOR FILING DATE: 2004-05-03
 ; NUMBER OF SEQ ID NOS: 673904
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO: 210506

Query Match 4.3%; Score 17.8; DB 12; Length 25;
 Best Local Similarity 90.5%; Pred. No. 2.8e+05;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 144 CAAAGTTGAGAAGCTAATA 164
 Db 22 CAAAGGTGAGAAGCTAATA 2

RESULT 14
 US-11-121-849-210507/C
 ; Sequence 210507, Application US/11121849
 ; Publication No. US20050272080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John Palma
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Samples
 ; FILE REFERENCE: 3684.1
 ; CURRENT APPLICATION NUMBER: US/11/121,849
 ; CURRENT FILING DATE: 2005-05-03
 ; PRIOR APPLICATION NUMBER: 60/567,949
 ; PRIOR FILING DATE: 2004-05-03
 ; NUMBER OF SEQ ID NOS: 673904
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO: 210507
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-11-121-849-210507

Query Match 4.3%; Score 17.8; DB 12; Length 25;
 Best Local Similarity 90.5%; Pred. No. 2.8e+05;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 144 CAAAGTTGAGAAGCTAATA 164
 Db 21 CAAAGGTGAGAAGCTAATA 1

RESULT 15
 US-10-932-182A-145807
 ; Sequence 145807, Application US/10932182A
 ; Publication No. US20060046253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAO, YOSHIIRO
 ; APPLICANT: NAKAMURA, NORIHIRO
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOSHIKI
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 ; FILE REFERENCE: 030e85-043
 ; CURRENT APPLICATION NUMBER: US/10/932-182A
 ; CURRENT FILING DATE: 2004-09-02
 ; NUMBER OF SEQ ID NOS: 19/023
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO: 145807
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces pastorianus
 US-10-932-182A-145807

Query Match 4.3%; Score 17.6; DB 7; Length 25;
 Best Local Similarity 83.3%; Pred. No. 3.1e+05;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 60 TTGTGCGCTTAGTAGAAGCTTGG 83
 Db 2 TTGTGCGCTAACCGAAGCTTGG 25

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US-08-664-856A-8
 Query Match 5.8%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TATCGCTAGGGCTGACCGCG 24
 Db 1 TATCGCTAGGGCTGACCGCG 24

RESULT 2
 US-08-664-856A-9/c
 Sequence 9, Application US/08664856A

Patent No. 5663071
 GENERAL INFORMATION:
 APPLICANT: BRUCE R. ZETTER AND LERE BAO
 TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
 TITLE OF INVENTION: PROTEIN AND USES THEREOF
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02119

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatibile
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,796
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 4,6507
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 US-08-801-796-8

Query Match 5.8%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TATCGCTAGGGCTGACCGCG 24
 Db 1 TATCGCTAGGGCTGACCGCG 24

RESULT 4
 US-08-801-796-9/c
 Sequence 9, Application US/08801796
 Patent No. 5721337
 GENERAL INFORMATION:
 APPLICANT: BRUCE R. ZETTER AND LERE BAO
 TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
 TITLE OF INVENTION: PROTEIN AND USES THEREOF
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02119

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatibile
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,796
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 4,6507
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 US-08-801-796-9

RESULT 3
 US-08-801-796-8
 Sequence 8, Application US/08801796
 Patent No. 5721337

OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 FILING DATE: 14-FEB-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/664,856
 FILING DATE: 17 JUN 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 46507
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEX: 200291 STRB
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 US-08-931-877-8

Query Match Score 5.8%; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 24;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 ACCCTGACTGAAGGTAGCATT 379
 Db 24 ACCCTGACTGAAGGTAGCATT 1

RESULT 5
 US-08-931-877-8
 Sequence 8, Application US/08931877
 Patent No. 5831033
 GENERAL INFORMATION:
 APPLICANT: BRUCE R. ZETTER AND LERE BAO
 TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02019
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,877
 FILING DATE: 17-SEP-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 46507
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEX: 200291 STRB
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/069,484
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/801,796
 FILING DATE: 14-FEB-1997
 APPLICATION NUMBER: 08/664,856
 FILING DATE: 17 JUN 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEX: 617-523-6440
 TELEX: 200291 STRE

SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 US-09-069-484-9

Query Match 5.8%; Score 24; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 356 ACCCTGACTGAAAGTCAGCATT 379
 Db 24 ACCCTGACTGAAAGTCAGCATT 1

RESULT 11
 US-09-135-599-3
 Sequence 3, Application US/0913599
 Patent No. 6150117

GENERAL INFORMATION:
 APPLICANT: BRUCE R. ZETTER AND LERE BAO
 TITLE OF INVENTION: A METHOD FOR DIAGNOSIS AND PROGNOSIS OF
 CANCER
 NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02019

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTSEQ Version 1.5

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/135,599
 FILING DATE: 18 AUG 1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/664,857
 FILING DATE: 17 JUN 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REGISTRATION NUMBER: 34,235
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEX: 200291 STRE

SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/801,796
 FILING DATE: 14-FEB-1997
 APPLICATION NUMBER: 08/664,856
 FILING DATE: 17 JUN 1996

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: 
; ORIGINAL SOURCE: US-09-135-599-3

Query Match      5.8t;  Score 24;  DB 3;  Length 24;
Best Local Similarity 100.0%;  Pred. No. 7.6e+02;
Matches 24;  Conservative 0;  Mismatches 0;  Indels 0;

Qy      1 TATCAGCTAGTCAGTCGACCCGCG 24
Db      1 TATCAGCTAGTCAGTCGACCCGCG 24

RESULT 12
US-09-135-599-4/c
; Sequence 4, Application US/09135599
; Patent No. 6510017
; GENERAL INFORMATION:
;   APPLICANT: BRUCE R. ZETTER AND LERE BAO
;   TITLE OF INVENTION: A METHOD FOR DIAGNOSIS AND PROGNOSIS OF
;   TITLE OF INVENTION: CANCER
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;     STREET: 130 WATER STREET
;     CITY: BOSTON
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02019
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FABSEQ Version 1.5
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/135,599
;   FILING DATE: 18 AUG 1998
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/664,857
;     FILING DATE: 17 JUN 1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME: DAVID, RESNICK S
;       REGISTRATION NUMBER: 34,235
;       REFERENCE/DOCKET NUMBER: 46403
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-523-3400
;     TELEFAX: 617-523-6440
;     TELEX: 200291 STRE
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 24 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       FRAGMENT TYPE: 
;       ORIGINAL SOURCE: 
;   US-09-135-599-4

Query Match      5.8t;  Score 24;  DB 3;  Length 24;
Best Local Similarity 100.0%;  Pred. No. 7.6e+02;
Matches 24;  Conservative 0;  Mismatches 0;  Indels 0;

Qy      356 ACCCTGACTGAAAGTCAGCATT 379
Db      24 ACCCTGACTGAAAGTCAGCATT 1

```

RESULT 13
US-09-369-744-8
Sequence 8, Application US/09369744
Patent No. 6300479
GENERAL INFORMATION:
APPLICANT: BRUCE R. ZETTER AND LERE BAO
TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
TITLE OF INVENTION: PROTEIN AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FABESBQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/369,744
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,796
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-09-369-744-8

Query Match 5.8%; Score 24; DB 3; Local Similarity 100.0%; Pred. No. 7.6e+02; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 24; Conservative 0; Mismatches 0;

Qy	Db	Score	DB	Local Similarity	Conservative	Mismatches
1	1	TATCAGCTAGTGGCTGCACCGCG	24			
1	1	TATCAGCTAGTGGCTGCACCGCG	24			

RESULT 14
US-09-369-744-9/C
Sequence 9, Application US/09369744
Patent No. 6300479
GENERAL INFORMATION:
APPLICANT: BRUCE R. ZETTER AND LERE BAO
TITLE OF INVENTION: HUMAN THYMOSIN 15 GENE,
TITLE OF INVENTION: PROTEIN AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA

ZIP: 02019
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION NUMBER: US/09/369,744
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/801,796
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: DAVID, RESNICK S
 REFERENCE/DOCKET NUMBER: 34,235
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 523-3400
 TELEFAX: 617-523-6440
 TELEX: 200291 STRE
 SEQUENCE FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 US-09-369-744-9

Query Match 5.8%; Score 24; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 356 ACCCTGACTGAAAGTCAGCATT 379
 Db 24 ACCCTGACTGAAAGTCAGCATT 1

RESULT 15
 US-08-411-796-374-C
 Sequence 374, Application US/08411796
 Patent No. 577149
 GENERAL INFORMATION:
 APPLICANT: Abrams, Mark A.
 APPLICANT: Bauer, S. C.
 APPLICANT: Bradford-Goldberg, Sarah R.
 APPLICANT: Caparon, Maire H.
 APPLICANT: Easton, Alan M.
 APPLICANT: Klein, Barbara K.
 APPLICANT: McKearn, John P.
 APPLICANT: Ollins, Peter O.
 APPLICANT: Paik, Kunman
 APPLICANT: Polazzi, Joseph O.
 APPLICANT: Thomas, John W.

TITLE OF INVENTION: Inter-leukin-3 (IL-3) Mutant Polypeptides

CORRESPONDENCE ADDRESS: 549
 ADDRESSE: Dennis A. Bennett, G.D. Searle & Co.,
 ADDRESS: Corporate Patent Dept.
 STREET: P. O. Box 5110
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60680
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/411,796
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/981044
 FILING DATE: 24-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/11198
 FILING DATE: 22-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Dennis A.
 REGISTRATION NUMBER: 34,547
 REFERENCE/DOCKET NUMBER: C2713/1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (708) 470-6501
 TELEFAX: (708) 470-6881
 INFORMATION FOR SEQ ID NO: 374:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 36 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (synthetic)
 US-08-411-796-374
 Query Match 5.0%; Score 20.4; DB 2;
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 181 TCTTCCTTCGAGGAAACTATCCAGCAGGA 210
 Db 31 TGTTCCTTCGAGGTTATTCATCAGGA 2
 Job time : 155 secs

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